

CLAIMS

1. A method for screening a test compound for anti-neoplastic activity, the method comprising: providing a cell, measuring expression by the cell of a plurality of genes selected from Table 1, exposing the cell to the test compound, and re-measuring the expression by the cell of the plurality of genes, wherein the degree of increase in expression of the plurality of genes corresponds to the degree of anti-neoplastic activity of the test compound.
2. The method of claim 1 wherein the degree of increase of expression of the plurality of genes is measured using a weighted average.
3. The method of claim 1 wherein the plurality of genes comprises at least 20 genes selected from Table 1.
4. The method of claim 1 wherein the plurality of genes comprises at least 50 genes selected from Table 1.
5. The method of claim 1 wherein the plurality of genes comprises at least 121 genes selected from Table 1.
6. The method of claim 1 wherein the plurality of genes comprises at least 123 genes selected from Table 1.
7. The method of claim 1 wherein the plurality of genes comprises PKA, TOB1, ERBIN, NIP3, TSP1, BUB1B, TTK, PSMC6, and USP1.
8. The method of claim 1 wherein the plurality of genes comprises genes selected from the group consisting of: genes that regulate apoptosis, genes involved in suppression of cell proliferation, mitotic check point genes, genes involved in protein degradation, and genes that up-regulate the gap junction proteins.

9. The method of claim 1 wherein gene expression is measured using an array comprising a substrate and a plurality of polynucleotide probes affixed to the substrate.
10. The method of claim 9 wherein the array comprises a plurality of polynucleotide probes that are specifically complementary to a plurality of genes as shown in Table 1.
11. The method of claim 10 wherein the polynucleotide probes are specifically complementary to at least 20 genes selected from Table 1.
12. The method of claim 10 wherein the polynucleotide probes are specifically complementary to at least 121 genes selected from Table 1.
13. A method for monitoring the efficacy of a prophylactic treatment of a subject, the subject having at least one risk factor for a neoplastic disease, the method comprising administering to the subject a therapeutic compound, and measuring the change in expression of a plurality of genes selected from Table 1.
14. The method of claim 13 wherein the therapeutic compound is lunasin or a compound related to or derived from lunasin.
15. The method of claim 13 wherein the plurality of genes comprises at least 20 genes selected from Table 1.
16. The method of claim 13 wherein the plurality of genes comprises at least 50 genes selected from Table 1.
17. The method of claim 13 wherein the plurality of genes comprises at least 121 genes selected from Table 1.

18. The method of claim 13 wherein the plurality of genes comprises at least 123 genes selected from Table 1.
19. The method of claim 13 wherein the plurality of genes comprises PKA, TOB1, ERBIN, NIP3, TSP1, BUB1B, TTK, PSMC6, and USP1.
20. The method of claim 13 wherein the plurality of genes comprises genes selected from the group consisting of: genes that regulate apoptosis, genes involved in suppression of cell proliferation, mitotic check point genes, genes involved in protein degradation, and genes that up-regulate the gap junction proteins.
21. A method for monitoring the efficacy of a treatment of a subject, the subject having a neoplastic disease, the method comprising administering to the subject a therapeutic compound, and measuring the change in expression of a plurality of genes selected from Table 1.
22. The method of claim 21 wherein the therapeutic compound is lunasin or a compound related to or derived from lunasin.
23. The method of claim 21 wherein the plurality of genes comprises at least 20 genes selected from Table 1.
24. The method of claim 21 wherein the plurality of genes comprises at least 50 genes selected from Table 1.
25. The method of claim 21 wherein the plurality of genes comprises at least 121 genes selected from Table 1.
26. The method of claim 21 wherein the plurality of genes comprises at least 123 genes selected from Table 1.

27. An array comprising a substrate to which is bound a plurality of polynucleotide probes that are specifically complementary to one or more genes as shown in Table 1.
28. The array of claim 27 wherein the polynucleotide probes are specifically complementary to at least 20 genes selected from Table 1.
29. The array of claim 27 wherein the polynucleotide probes are specifically complementary to at least 50 genes selected from Table 1.
30. The array of claim 27 wherein the polynucleotide probes are specifically complementary to at least 121 genes selected from Table 1.
31. The array of claim 27 wherein the polynucleotide probes are specifically complementary to at least 123 genes selected from Table 1.
32. The array of claim 27 wherein the polynucleotide probes comprise probes complimentary to PKA, TOB1, ERBIN, NIP3, TSP1, BUB1B, TTK, PSMC6, and USP1.
33. The method of claim 27 wherein the polynucleotide probes comprise probes complimentary to genes selected from the group consisting of: genes that regulate apoptosis, genes involved in suppression of cell proliferation, mitotic check point genes, genes involved in protein degradation, and genes that up-regulate the gap junction proteins.